Amendments to the Specification:

Please replace the paragraph beginning at page 26, line 19, with the following:

--FIG. 12 illustrates the increase in relative abundance for peaks corresponding to the acetylated peptide masses, with increasing nozzle potential. Acetyl-SRPSLDQ = SEQ ID NO:6.--

Please replace the paragraph beginning at page 26, line 23, with the following:

--FIG. 14 provides the minimally fragmenting 12 V spectrum of PITC-Bradykinin peptide (SEQ ID NO:7). A zero charge mass deconvolution of the multiply charged mass peaks observed between 700 and 4000 amu was prepared using the BioSpec Data Explorer™ software.--

Please replace the paragraph beginning at page 26, line 29, with the following:

--FIG. 16 provides an example of a substantially fragmented mass spectra, corresponding to 250 V nozzle potential for PITC-labeled Bradykinin (SEQ ID NO:7).--

Please replace the paragraph beginning at page 26, line 31, with the following:

--FIGS. 17 and 18 illustrate the peak counts corresponding to the a-ions (Figure 17) and b-ions (Figure 18) generated from the IMB-labeled peptide fragment (SEQ ID NO:8) masses were clearly observed to increase in relative abundance with increasing nozzle potential with a maximum fragmentation abundance noted at about 200V.--

Please replace the paragraph beginning at page 27, line 3, with the following:

--FIG. 19 shows the mass spectrum from SPITC-labeled apomyoglobin (SEQ ID NO:9) obtained in the negative ion mode. The nozzle potential was increased from a minimum setting of 125 V to a maximum of 300V in 25-50 V increments with 1 minute of instrument equilibration time allotted before collecting spectra at each nozzle potential. A total of thirty 3-second spectra were accumulated for analysis at each nozzle potential.--

Please replace the paragraph beginning at page 27, line 10, with the following:

--FIG. 21 shows the increase in relative abundance for the doubly charged y_{1-7} ions generated from the C-terminal (2-aminoethyl)trimethylammonium-labeled Bradykinin peptide (SEQ ID NO:10) obtained in positive ion mode. The nozzle potential was increased from a minimum of 50 V to a maximum of 300 V in 50 V increments with 1 minute of instrument equilibration time allotted before collecting spectra at each nozzle potential. A total of sixty 3-second spectra were accumulated for analysis at each nozzle potential.--

Please replace the paragraph beginning at page 99, line 11, with the following:

--The identity and purity of the parent glycogen phosphorylase A protein was determined at the minimally fragmenting 12 V spectrum (Figure 1) by conducting a zero charge mass deconvolution of the multiply charged mass peaks observed between 700 and 4000 amu using the BioSpec Data Explorer™ software (Version 3.0) supplied by the vendor. The N-terminal sequence of glycogen phosphorylase was determined by inspecting the resulting mass spectra to determine the relative abundance of the possible acetylated peptides at each nozzle potential. Peaks corresponding to the acetylated peptide masses were clearly observed to increase in relative abundance with increasing nozzle potential (Figure 12). Figure 12 shows the

cumulative relative abundance of both the a- and b-ions for each peptide mass in the sequence. An example of a substantially-fragmented mass spectra, corresponding to 250V nozzle potential of 250 V is shown in Figure 13. Those mass fragments showing increased abundance at nozzle potentials above 200V correspond to the published amino-terminal sequence for glycogen phosphorylase, acetyl-SRPLSD (SEQ ID NO:11) (see Persson, et al., *ibid.*).--

Please cancel the present "SEQUENCE LISTING", pages 1-2, submitted March 9, 2006, and insert therefor the accompanying paper copy of the Substitute Sequence Listing, page numbers 1 to 4, at the end of the application.